

R. Shukla

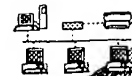
RAW SEQUENCE LISTING
ERROR REPORT

RECEIVED

APR 30 2001

TECH CENTER 1600/2900

BIOTECHNOLOGY
SYSTEMS
BRANCH



5-1-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/465,978
Source: 1632
Date Processed by STIC: 4-17-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/465, 978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:13

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

3 <110> APPLICANT: Zhang, Ning and Anthony Purchio
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS
 6 MODULATING COMPOUNDS
 8 <130> FILE REFERENCE: PXE-012.US
 10 <140> CURRENT APPLICATION NUMBER: US/09/465,978
 11 <141> CURRENT FILING DATE: 1999-12-16
 13 <150> PRIOR APPLICATION NUMBER: 60/152,522
 14 <151> PRIOR FILING DATE: 1999-09-03
 16 <160> NUMBER OF SEQ ID NOS: 51
 18 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
 Corrected Diskette Needed
 see pp. 1-2-4

ERRORED SEQUENCES

531 <210> SEQ ID NO: 40
 532 <211> LENGTH: 7093
 533 <212> TYPE: DNA
 534 <213> ORGANISM: Mus sp.
 536 <400> SEQUENCE: 40
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 538 cacacaatgc ttggttttgt tottcaactt ttctgttat gatgcagtc ctggtttgtg 120
 539 taactatgag cttcaaaagc aaagaacgca tcatctattt ttgtgtctct tcttccaagg 180
 540 acttagtgta tcacttactg gctaaatgct tgagacaaaa acagggatta atgaagaaga 240
 541 aagagaaaaga aaagggaagg aaagtgccca caattactga cagggtttca gtaaagcagt 300
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 564 tgtgctaagt cttggagatt tagtggtgaa gaagtcaggt gtgtttccaa tctcatggag 1680

Missing mandatory <220> to <223> features
 to explain the "n" at position 3617 in
 Seq. #40. (See next page)

Also see #10
 on the Error
 Summary Sheet.

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:13

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

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567 gtggtcttca aagacccttt agaagctgag aactaaagac agcaagcaag gtgagggcag 1860
568 catctccacc tttccagtgg aatgagcaac ttagggtata cagctgattc ccacattgtc 1920
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574 catgattaac ttcaatttat acctgtaagt tataccacat cctaaacacg ctgatgtccc 2280
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→ see p.1
explanation.

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:13

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Output Set: N:\CRF3\04172001\I465978.raw

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655 ctggggaagt atg 7093

```

09/465, 978
End of
Seg. #51 (partially shown)

p. 4

```
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PXE-012.US

2

→ Delete extraneous material from
the end of the file. It is causing
a program error.

VERIFICATION SUMMARY

DATE: 04/17/2001

PATENT APPLICATION: US/09/465,978

TIME: 13:03:14

Input Set : A:\PXE-012.US seqlist.txt

Output Set: N:\CRF3\04172001\I465978.raw

L:597 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40

L:1066 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1

L:1068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:51